```
<!--StartFragment-->GenCore version 6.2.1
                Copyright (c) 1993 - 2008  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          April 29, 2008, 13:52:39 ; Search time 11061 Seconds
                                           (without alignments)
                                           17362.216 Million cell updates/sec

Title:           US-10-532-944-7
Perfect score:   2346
Sequence:        1 gtgggcatgattcacgagca.........cgttttccatccatgtgtga 2346

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters:      19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_env:*
                 2:  gb_pat:*
                 3:  gb_ph:*
                 4:  gb_pl:*
                 5:  gb_pr:*
                 6:  gb_ro:*
                 7:  gb_sts:*
                 8:  gb_sy:*
                 9:  gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_in:*
                 13: gb_om:*
                 14: gb_ba:*
                 15: gb_htg1:*
                 16: gb_htg2:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
                    Query
Result      Score  Match Length DB  ID                        Description
  No.
-----------------------------------------------------------------------------
    1       2346   100.0   8690  14  AJ252161                  AJ252161 Alicyclob
    2       2187    93.2   2187   2  DD448952                  DD448952 GLUCOSIDA
    3       1002    42.7   3097  14  AJ133789                  AJ133789 Alicyclob
    4      597.2    25.5   3854  14  AB012238                  AB012238 Bacillus
    5      427.4    18.2 110000  14  CP000386_21               Continuation (22 o
    6      423.2    18.0 110000  14  AE017262_01               Continuation (2 of
```

```
        7     423   18.0 110000  14 CP000239_22           Continuation (23 o
        8     423   18.0 110000  14 CP000239_23           Continuation (24 o
        9   416.8   17.8 110000   2 BD455614_01           Continuation (2 of
       10   416.8   17.8 200050  14 AL591973              AL591973 Listeria
       11   416.8   17.8 349980   2 AX638811              AX638811 Sequence
       12     412   17.6    7787   2 AX416892              AX416892 Sequence
       13     409   17.4 231450  14 AL596163              AL596163 Listeria
       14     409   17.4 349980   2 AX415067              AX415067 Sequence
       15     409   17.4 349980   2 AX453571              AX453571 Sequence
       16   384.6   16.4 110000  14 CP000240_14           Continuation (15 o
c      17   379.4   16.2 110000  14 BA000045_01           Continuation (2 of
c      18   360.4   15.4 110000  14 CP000360_07           Continuation (8 of
c      19   360.4   15.4 110000  14 CP000360_08           Continuation (9 of
       20     344   14.7 110000  14 CP000411_07           Continuation (8 of
       21   337.2   14.4    2259  14 EF635970              EF635970 Thermoana
       22   332.6   14.2 304274  14 AL935262              AL935262 Lactobaci
       23   319.8   13.6    2301   2 DD459592              DD459592 Lactobaci
c      24   319.8   13.6 110000  14 CP000033_18           Continuation (19 o
c      25   319.8   13.6 110000  14 CP000413_17           Continuation (18 o
       26   319.6   13.6    9699  14 AE012974              AE012974 Thermoana
       27   312.4   13.3 110000  14 BA000019_56           Continuation (57 o
       28   299.8   12.8 110000  14 BA000045_16           Continuation (17 o
       29   299.8   12.8 110000  14 CP000721_16           Continuation (17 o
       30   290.8   12.4 110000  14 CP000383_08           Continuation (9 of
       31   290.8   12.4 110000  14 CP000383_09           Continuation (10 o
       32   284.4   12.1 232605  14 AE017222              AE017222 Thermus t
c      33   282.4   12.0 110000  14 BA000030_83           Continuation (84 o
       34   281.2   12.0    2328   2 BD179690              BD179690 Highly th
       35   281.2   12.0 256992  14 AP008227              AP008227 Thermus t
c      36   280.6   12.0 110000  14 AE017198_18           Continuation (19 o
       37   280.6   12.0 349980   2 AX926712              AX926712 Sequence
       38   280.6   12.0 349980   2 AX926713              AX926713 Sequence
       39     278   11.8    2703   2 DD355846              DD355846 Dextrinde
       40   276.2   11.8    2307  14 DQ857783              DQ857783 Lactobaci
       41     268   11.4 110000  14 CP000685_32           Continuation (33 o
       42   263.8   11.2    2926   6 BC117889              BC117889 Mus muscu
       43   263.8   11.2    3484   4 AK243062              AK243062 Oryza sat
       44   262.2   11.2    2923   6 BC117888              BC117888 Mus muscu
       45   262.2   11.2    2998   6 BC128069              BC128069 Mus muscu


                               ALIGNMENTS


RESULT 1
AJ252161
LOCUS       AJ252161              8690 bp    DNA     linear   BCT 15-APR-2005
DEFINITION  Alicyclobacillus acidocaldarius maltose/maltodextrine transport
            gene region (malEFGR genes, cdaA gene and glcA gene).
ACCESSION   AJ252161
VERSION     AJ252161.1  GI:6686561
KEYWORDS    alpha-glucosidase; cdaA gene; cyclomaltodextrinase; glcA gene; malE
            gene; malF gene; malG gene; MALR gene; maltose binding protein;
            maltose transport membrane protein; repressor of maltose transport
            genes.
SOURCE      Alicyclobacillus acidocaldarius
  ORGANISM  Alicyclobacillus acidocaldarius
            Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
            Alicyclobacillus.
REFERENCE   1
  AUTHORS   Hulsmann,A., Lurz,R., Scheffel,F. and Schneider,E.
```

```
   TITLE     Maltose and maltodextrin transport in the thermoacidophilic
             gram-positive bacterium Alicyclobacillus acidocaldarius is mediated
             by a high-affinity transport system that includes a maltose binding
             protein tolerant to low pH
   JOURNAL   J. Bacteriol. 182 (22), 6292-6301 (2000)
   PUBMED    11053372
REFERENCE    2  (bases 1 to 8690)
   AUTHORS   Huelsmann,A.
   TITLE     Direct Submission
   JOURNAL   Submitted (06-JAN-2000) Huelsmann A., Bakterienphysiologie,
             Humboldt Universitaet zu Berlin, Chausseestr. 117, 10115 Berlin,
             GERMANY
FEATURES             Location/Qualifiers
     source          1. .8690
                     /organism="Alicyclobacillus acidocaldarius"
                     /mol_type="genomic DNA"
                     /strain="ATCC 27009"
                     /db_xref="taxon:405212"
     gene            133. .1416
                     /gene="malE"
     CDS             133. .1416
                     /gene="malE"
                     /function="maltose tranport"
                     /codon_start=1
                     /transl_table=11
                     /product="maltose binding protein"
                     /protein_id="CAB65651.1"
                     /db_xref="GI:6686562"
                     /db_xref="GOA:Q9RHZ6"
                     /db_xref="InterPro:IPR006059"
                     /db_xref="InterPro:IPR006060"
                     /db_xref="PDB:1URD"
                     /db_xref="PDB:1URG"
                     /db_xref="PDB:1URS"
                     /db_xref="UniProtKB/TrEMBL:Q9RHZ6"
                     /translation="MSVRRWGIVSTGVAALVLAGGAIAGCGTSNGGQNTSPSTSSSSA
                     KGEASALPKGQTITVWSWQTGPELQDVKQIAAQWAKAHGDKVIVVDQSSNPKGFQFYA
                     TAARTGKGPDVVFGMPHDNNGVFAEEGLMAPVPSGVLNTGLYAPNTIDAIKVNGTMYS
                     VPVSVQVAAIYYNKKLVPQPPQTWAEFVKDANAHGFMYDQANLYFDYAIIGGYGGYVF
                     KDNNGTLDPNNIGLDTFGAVQAYTLMRDMVSKYHWMTPSTNGSIAKAEFLAGKIGMYV
                     SGPWDTADIEKAKIDFGVTPWPTLPNGKHATPFLGVITAFVNKESKTQAADWSLVQAL
                     TSAQAQQMYFRDSQQIPALLSVQRSSAVQSSPTFKAFVEQLRYAVPMPNIPQMQAVWQ
                     AMSILQNIIAGKVSPEQGAKDFVQNIQKGIMAQGS"
     sig_peptide     133. .210
                     /gene="malE"
     mat_peptide     211. .1413
                     /gene="malE"
                     /product="MalE"
     gene            1483. .2448
                     /gene="malF"
     CDS             1483. .2448
                     /gene="malF"
                     /citation=[1]
                     /codon_start=1
                     /transl_table=11
                     /product="putative maltose transport membrane protein"
                     /protein_id="CAB65652.1"
                     /db_xref="GI:6686563"
                     /db_xref="GOA:Q9RHZ5"
                     /db_xref="InterPro:IPR000515"
                     /db_xref="UniProtKB/TrEMBL:Q9RHZ5"
```

```
                        /translation="MATVMEMRRSHGRERAKRRVDWVAYGYLSPALVTICVLSILPIF
                        YTIYISFTNFNQMHFLSYQFVGLKNYEELLNPHDPLSNLFLPTFIWTLVYALCTTALA
                        YLVGLFLAVLLNNKHMRERTLYRTLLIVPWAVPNLISMLAWQGLLNDQYGQINALLHG
                        VFGLPRIPWLTSALWARIAVIMVNVWAGFPYMMTVCLGALQSIPTDQYEAAEIDGANW
                        WQVFRYVTMPSVWRISLPLLIPSFSYNFNNFNASYLLTGGGPPNSNNPFLGQTDILAT
                        AAYKMTLTFNRYDLGATISVLLFILVALISWVQMRYTGAFKEVDA"
gene                    2448. .3353
                        /gene="malG"
CDS                     2448. .3353
                        /gene="malG"
                        /citation=[1]
                        /codon_start=1
                        /transl_table=11
                        /product="putative maltose transport membrane protein"
                        /protein_id="CAB65653.1"
                        /db_xref="GI:6686564"
                        /db_xref="GOA:Q9RHZ4"
                        /db_xref="InterPro:IPR000515"
                        /db_xref="UniProtKB/TrEMBL:Q9RHZ4"
                        /translation="MAMSSQSFSAMKSQRPIAARTRRRRSMQPGEQVALWVSRIVIWC
                        VIVMVLLPMWFVVIASFNPSNSYISFSLFPSNASLANYKALFQGGQFWTWVRNSLVVG
                        VVVAMAQSFITAMSAFAFSKLRFYGRKYGLMTLLLLQMFPNILAIAAFYTALAKLNMI
                        DMLGSYILVMLGTSAFNIWLLKGYMDSVPKELDEAAVIDGATTWQRFIHVTLPLSTPM
                        MVVIFFLTLVGIFSEYMFAGTILQSPWNYTLGVGMYNLISGQFAKNWGEFAAAALLSA
                        VPLAIVFAVAQRYLTKGLVAGSVKG"
gene                    3379. .4407
                        /gene="malR"
CDS                     3379. .4407
                        /gene="malR"
                        /citation=[1]
                        /codon_start=1
                        /transl_table=11
                        /product="putative repressor of maltose transport genes"
                        /protein_id="CAB65654.1"
                        /db_xref="GI:6686565"
                        /db_xref="GOA:Q9RHZ3"
                        /db_xref="HSSP:P03023"
                        /db_xref="InterPro:IPR000843"
                        /db_xref="InterPro:IPR001761"
                        /db_xref="InterPro:IPR010982"
                        /db_xref="UniProtKB/TrEMBL:Q9RHZ3"
                        /translation="MATIKDVARLANVSPSTVSRVLANSPRISEETKRRVRAALEQLN
                        YHPNAFARGLVTNSTGAIGILIPPSAQEFFVNPFFAEWMAGVAEVARQRGVDTVLSTS
                        ARGEIETLDHMIRGRRVDGVLLIGARQGDPVLQEVAKLRCPAVLLGRPADPAPISWVN
                        NDNQRAAYDATVHLLNLGHRRIGFLGGASDLVVTMDRVAGYRQALVDHGVEPDSRLEV
                        SSFFLEQGGYLGMMRLLAIPDRPTAVLCADDVLAFGGMRAAHELGFEVPGDLAIVGFN
                        DIRLAELAHPALTSVRVHMHELGVRSAELLLEEIDQGKPLQRHVIVKHELVIRYSCGA
                        KPIGTLTT"
gene                    4434. .6170
                        /gene="cdaA"
CDS                     4434. .6170
                        /gene="cdaA"
                        /function="linearises cyclomaltodextrines"
                        /citation=[1]
                        /codon_start=1
                        /transl_table=11
                        /product="cyclomaltodextrinase"
                        /protein_id="CAB65655.1"
                        /db_xref="GI:6686566"
                        /db_xref="GOA:Q9WX32"
                        /db_xref="HSSP:P38940"
```

```
                        /db_xref="InterPro:IPR004185"
                        /db_xref="InterPro:IPR006047"
                        /db_xref="InterPro:IPR006589"
                        /db_xref="UniProtKB/TrEMBL:Q9WX32"
                        /translation="MELVWQHRWAADAYPLDLSTMVLVLRVARCTPAQRVRVHFGDRY
                        EPDFQNSSEARRYGSDGTFDWFTCRVAAPTRRLKYAFEVLSSTGRAVYLGEGGLADTL
                        DAVQPFQYPYIHPSRVLAVPDWVGHAVAYQIFPDRFAVGEQQLVRPTDPWDARPTPDS
                        VFGGNLRGIVDKLPYLSDLGVNLMYLTPIFQAPSNHKYDTQDYFAVDPAFGTLGDLQL
                        LVREAHRLGIRVVLDAVFNHSGFQFAPFQDVIARGTASPYWSWFFVQGDRVDVESVNY
                        ETFATRLRHMPKLNLAEPAAEEYFLQVAKHYVLECDIDGWRFDVANEIDPHFWSRLRS
                        ELRALKPDILLIGEIWHDSLPWLMGDAFDGVMNYPLRELVMRYAMDESIDEPAFAEAW
                        VRLYLQYPRPAWRAMWNLLGSHDTERALTRARGHVPSVVLAFAMLFTLPGIPMVYYGD
                        EIGMEGGTDPDCRRGMIWDANLWQLDLREAVRQLAWLKRTHPALAGDTMEIRDANSGV
                        LHYVRLNGTGPHLHIAVCKRRDFGAEVDSPLFAWDVPSRTSGEERKILIWECDSTEGC
                        GHDSRADGFHNQ"
        gene            6289. .8475
                        /gene="glcA"
        CDS             6289. .8475
                        /gene="glcA"
                        /citation=[1]
                        /codon_start=1
                        /transl_table=11
                        /product="putative alpha-glucosidase"
                        /protein_id="CAB65656.1"
                        /db_xref="GI:6686567"
                        /db_xref="GOA:Q9RHZ2"
                        /db_xref="HSSP:O59645"
                        /db_xref="InterPro:IPR000322"
                        /db_xref="UniProtKB/TrEMBL:Q9RHZ2"
                        /translation="MVGVAALDDTVLRVAYCRSPGEWPTSTPAIVEQMSQRHSWRLVQ
                        EERRVQLECVAGWQIQINRDDGTWSIRHLGFGTAVEAITWYKRKKGGALTFASLDNAR
                        FYGLGEKPGPLDKRHEAYTMWNSDVYAPHVPEMEALYLSIPFFLRLQDQTAVGIFVDN
                        PGRSRFDFRSRYPDVEISTERGGLDVYFIFGASLKDVIRRYTKLTGRMPMPPKWALGY
                        HQSRYSYETQSEVLSVAQTFVERDIPVDALYLDIHYMDGYRVFTFDERRFPDPARMCD
                        ELRKLGVRVVPIVDPGVKQDPEYPVYMDGLAHNHFCQTAEGQVYLGEVWPGLSAFPDF
                        ASEEVRAWWGKWHRVYTQMGIEGIWNDMNEPAVFNETKTMDVNVVHRGDGRLYTHGEV
                        HNLYGFWMAEATYRGLKAQLAGKRPFVLTRAGYSGIQRYAAVWTGDNRSFWEHMAMAI
                        PMVLNMGMSGIPLGGPDVGGFAHHASGELLARWTQMGAFFPFFRNHSAMGTHRQEPWA
                        FGPTFEAVIRRAIRLRYRFLPYLYTLAREAHETGLPMMRPLVLEYPDDPNTHHVDDQF
                        LVGSDLLVAPILKPGMAHRMVYLPDGEWIDYETRERYQGRQYILTYAPLDRIPLYVRA
                        GSAIPVNLLERSGETQLGWEIFVDANGRASGRCYEDDGETFSYEDGAYCDRVLQALAT
                        SEGTLIECHLVQGSGDGGSLESVVRVFTPDDVREARAQGISFSIHV"
ORIGIN
```

Query Match   100.0%; Score 2346; DB 14; Length 8690;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2346; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 GTGGGCATGATTCACGAGCAGACGGATTTCACAACCAGTGAGGCGATCCGCCCGGATACG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6130 GTGGGCATGATTCACGAGCAGACGGATTTCACAACCAGTGAGGCGATCCGCCCGGATACG 6189

Qy    61 CTGATCTCGCCGCCAGATGACTGGGCTTTTCTCGGGCGACCCAGCCGGTTTGATGTGGAT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6190 CTGATCTCGCCGCCAGATGACTGGGCTTTTCTCGGGCGACCCAGCCGGTTTGATGTGGAT 6249

Qy   121 CACGATGGCTGGGCGACGGTTCAGTATGACGCTGGAGTCATGGTCGGTGTCGCCGCACTC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6250 CACGATGGCTGGGCGACGGTTCAGTATGACGCTGGAGTCATGGTCGGTGTCGCCGCACTC 6309

Qy   181 GACGACACCGTGCTACGCGTAGCCTACTGCAGGTCCCCTGGGGAGTGGCCGACGAGCACA 240
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6310  GACGACACCGTGCTACGCGTAGCCTACTGCAGGTCCCCTGGGGAGTGGCCGACGAGCACA 6369

Qy       241  CCTGCCATTGTGGAACAGATGTCGCAGCGGCACTCCTGGCGGCTCGTTCAGGAAGAGCGA 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6370  CCTGCCATTGTGGAACAGATGTCGCAGCGGCACTCCTGGCGGCTCGTTCAGGAAGAGCGA 6429

Qy       301  CGCGTGCAACTGGAATGTGTTGCCGGATGGCAGATTCAAATCAACCGGGACGACGGAACA 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6430  CGCGTGCAACTGGAATGTGTTGCCGGATGGCAGATTCAAATCAACCGGGACGACGGAACA 6489

Qy       361  TGGAGTATACGCCATCTCGGCTTTGGGACAGCCGTCGAGGCCATCACGTGGTACAAGCGC 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6490  TGGAGTATACGCCATCTCGGCTTTGGGACAGCCGTCGAGGCCATCACGTGGTACAAGCGC 6549

Qy       421  AAAAAAGGCGGCGCATTGACGTTTGCTTCGCTCGACAATGCCCGGTTCTATGGACTTGGC 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6550  AAAAAAGGCGGCGCATTGACGTTTGCTTCGCTCGACAATGCCCGGTTCTATGGACTTGGC 6609

Qy       481  GAAAAGCCGGGGCCCCTTGACAAGCGGCACGAGGCGTACACCATGTGGAATTCGGACGTT 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6610  GAAAAGCCGGGGCCCCTTGACAAGCGGCACGAGGCGTACACCATGTGGAATTCGGACGTT 6669

Qy       541  TACGCGCCTCACGTGCCAGAGATGGAGGCCCTATACCTGTCGATCCCGTTCTTTTTGCGA 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6670  TACGCGCCTCACGTGCCAGAGATGGAGGCCCTATACCTGTCGATCCCGTTCTTTTTGCGA 6729

Qy       601  TTGCAAGACCAAACGGCCGTTGGCATCTTTGTGGATAATCCAGGGCGATCCCGCTTTGAC 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6730  TTGCAAGACCAAACGGCCGTTGGCATCTTTGTGGATAATCCAGGGCGATCCCGCTTTGAC 6789

Qy       661  TTCAGGAGCAGATACCCTGACGTGGAAATATCGACAGAACGAGGCGGGTTGGACGTTTAT 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6790  TTCAGGAGCAGATACCCTGACGTGGAAATATCGACAGAACGAGGCGGGTTGGACGTTTAT 6849

Qy       721  TTCATCTTCGGGGCTTCGCTCAAAGATGTCATTCGACGTTACACAAAGCTCACGGGGCGA 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6850  TTCATCTTCGGGGCTTCGCTCAAAGATGTCATTCGACGTTACACAAAGCTCACGGGGCGA 6909

Qy       781  ATGCCGATGCCACCCAAGTGGGCGCTCGGCTATCATCAGTCTCGGTACTCGTACGAGACC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6910  ATGCCGATGCCACCCAAGTGGGCGCTCGGCTATCATCAGTCTCGGTACTCGTACGAGACC 6969

Qy       841  CAGAGCGAGGTCCTGTCGGTGGCGCAAACGTTTGTCGAGCGCGACATTCCGGTGGATGCC 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6970  CAGAGCGAGGTCCTGTCGGTGGCGCAAACGTTTGTCGAGCGCGACATTCCGGTGGATGCC 7029

Qy       901  TTGTATCTGGATATTCACTACATGGATGGATATCGGGTGTTCACCTTTGATGAGAGGCGA 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7030  TTGTATCTGGATATTCACTACATGGATGGATATCGGGTGTTCACCTTTGATGAGAGGCGA 7089

Qy       961  TTTCCCGATCCGGCACGCATGTGCGACGAGTTGCGGAAGCTTGGGGTGCGCGTTGTCCCC 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7090  TTTCCCGATCCGGCACGCATGTGCGACGAGTTGCGGAAGCTTGGGGTGCGCGTTGTCCCC 7149

Qy      1021  ATCGTGGATCCGGGGGTGAAACAGGATCCTGAATATCCCGTTTACATGGACGGGCTAGCC 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7150  ATCGTGGATCCGGGGGTGAAACAGGATCCTGAATATCCCGTTTACATGGACGGGCTAGCC 7209

Qy      1081  CACAACCACTTCTGCCAAACCGCCGAGGGTCAAGTGTATCTTGGTGAGGTATGGCCCGGA 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    7210 CACAACCACTTCTGCCAAACCGCCGAGGGTCAAGTGTATCTTGGTGAGGTATGGCCCGGA 7269

Qy    1141 TTGAGTGCCTTTCCTGATTTCGCGTCGGAGGAAGTGCGGGCGTGGTGGGGCAAGTGGCAT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7270 TTGAGTGCCTTTCCTGATTTCGCGTCGGAGGAAGTGCGGGCGTGGTGGGGCAAGTGGCAT 7329

Qy    1201 CGGGTGTACACCCAGATGGGAATTGAGGGCATATGGAATGATATGAACGAGCCGGCTGTG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7330 CGGGTGTACACCCAGATGGGAATTGAGGGCATATGGAATGATATGAACGAGCCGGCTGTG 7389

Qy    1261 TTCAATGAGACGAAGACCATGGACGTGAACGTGGTCCACCGAGGCGACGGACGATTGTAC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7390 TTCAATGAGACGAAGACCATGGACGTGAACGTGGTCCACCGAGGCGACGGACGATTGTAC 7449

Qy    1321 ACGCACGGAGAGGTCCACAACCTCTATGGATTCTGGATGGCTGAAGCCACGTATCGCGGA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7450 ACGCACGGAGAGGTCCACAACCTCTATGGATTCTGGATGGCTGAAGCCACGTATCGCGGA 7509

Qy    1381 CTGAAAGCGCAGTTGGCTGGCAAGCGGCCTTTTGTGCTCACGCGCGCTGGCTACAGCGGA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7510 CTGAAAGCGCAGTTGGCTGGCAAGCGGCCTTTTGTGCTCACGCGCGCTGGCTACAGCGGA 7569

Qy    1441 ATTCAACGGTATGCGGCGGTGTGGACGGGCGACAACCGAAGCTTTTGGGAACATATGGCC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7570 ATTCAACGGTATGCGGCGGTGTGGACGGGCGACAACCGAAGCTTTTGGGAACATATGGCC 7629

Qy    1501 ATGGCCATCCCGATGGTGCTCAACATGGGGATGTCCGGTATTCCGCTCGGGGGCCCAGAT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7630 ATGGCCATCCCGATGGTGCTCAACATGGGGATGTCCGGTATTCCGCTCGGGGGCCCAGAT 7689

Qy    1561 GTGGGCGGTTTCGCTCATCACGCTTCAGGTGAATTGCTTGCACGATGGACGCAAATGGGG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7690 GTGGGCGGTTTCGCTCATCACGCTTCAGGTGAATTGCTTGCACGATGGACGCAAATGGGG 7749

Qy    1621 GCGTTCTTTCCGTTCTTTCGAAATCACAGTGCCATGGGAACGCATCGACAGGAACCTTGG 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7750 GCGTTCTTTCCGTTCTTTCGAAATCACAGTGCCATGGGAACGCATCGACAGGAACCTTGG 7809

Qy    1681 GCATTCGGCCCTACGTTCGAAGCCGTCATTCGACGTGCCATCCGGCTCCGTTATCGTTTC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7810 GCATTCGGCCCTACGTTCGAAGCCGTCATTCGACGTGCCATCCGGCTCCGTTATCGTTTC 7869

Qy    1741 CTGCCTTATCTGTACACGCTCGCACGGGAAGCCCATGAGACAGGTTTACCCATGATGCGG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7870 CTGCCTTATCTGTACACGCTCGCACGGGAAGCCCATGAGACAGGTTTACCCATGATGCGG 7929

Qy    1801 CCCTTGGTGTTAGAGTATCCCGACGATCCAAACACGCACCACGTCGATGATCAGTTCCTC 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7930 CCCTTGGTGTTAGAGTATCCCGACGATCCAAACACGCACCACGTCGATGATCAGTTCCTC 7989

Qy    1861 GTCGGTTCCGATCTTCTCGTGGCACCCATCCTCAAGCCGGGCATGGCCCATAGAATGGTC 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    7990 GTCGGTTCCGATCTTCTCGTGGCACCCATCCTCAAGCCGGGCATGGCCCATAGAATGGTC 8049

Qy    1921 TATTTGCCCGATGGAGAATGGATTGATTATGAGACGCGTGAGCGATACCAAGGGCGTCAG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8050 TATTTGCCCGATGGAGAATGGATTGATTATGAGACGCGTGAGCGATACCAAGGGCGTCAG 8109

Qy    1981 TACACATTGACGTATGCGCCTCTCGATCGTATCCCTCGTACGTGAGGGCAGGGAGCGCT 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8110 TACACATTGACGTATGCGCCTCTCGATCGTATCCCTCGTACGTGAGGGCAGGGAGCGCT 8169
```

```
Qy    2041 ATCCCCGTGAACCTCTTGGAGCGGTCGGGCGAGACCCAGCTAGGATGGGAGATCTTCGTG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8170 ATCCCCGTGAACCTCTTGGAGCGGTCGGGCGAGACCCAGCTAGGATGGGAGATCTTCGTG 8229

Qy    2101 GACGCCAACGGTCGAGCCTCGGGTCGATGCTATGAGGACGACGGCGAGACGTTTAGCTAT 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8230 GACGCCAACGGTCGAGCCTCGGGTCGATGCTATGAGGACGACGGCGAGACGTTTAGCTAT 8289

Qy    2161 GAAGACGGCGCCTACTGTGATCGCGTGTTACAGGCCCTCGCCACCTCGGAAGGAACACTG 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8290 GAAGACGGCGCCTACTGTGATCGCGTGTTACAGGCCCTCGCCACCTCGGAAGGAACACTG 8349

Qy    2221 ATCGAATGTCATCTTGTTCAAGGATCAGGAGATGGTGGAAGTCTCGAGAGCGTTGTTCGC 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8350 ATCGAATGTCATCTTGTTCAAGGATCAGGAGATGGTGGAAGTCTCGAGAGCGTTGTTCGC 8409

Qy    2281 GTGTTCACACCAGATGACGTTCGTGAGGCTCGTGCGCAGGGCATATCGTTTTCCATCCAT 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8410 GTGTTCACACCAGATGACGTTCGTGAGGCTCGTGCGCAGGGCATATCGTTTTCCATCCAT 8469

Qy    2341 GTGTGA 2346
           ||||||
Db    8470 GTGTGA 8475


<!--EndFragment-->
```